

# Camille Scott

## Permanent Address

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EDUCATION	<b>Alma College</b> , Alma, MI <i>B.S., Computer Science</i>	2008-2012
	<b>Michigan State University</b> , East Lansing, MI <i>DIB Lab, PhD. student, Computer Science</i>	2012-2015
	<b>University of California Davis</b> , Davis, CA <i>DIB Lab, PhD. student, Computer Science</i>	2015-present
HONOURS AND AWARDS	National Merit Finalist Alma College / Distinguished Scholar Award Binghamton University / Research Experience for Undergrads USDA / MSU/ National Needs Fellow	2008 2008-2012 summer 2011 2013-2015
MANUSCRIPTS	Scott, C. (2017). <i>shmlast: An improved implementation of Conditional Reciprocal Best Hits with LAST and Python</i> . The Journal of Open Source Software, 2017.  Ren, J., Chung-Davidson, Y. W., Yeh, C. Y., Scott, C., Brown, T., & Li, W. (2015). <i>Genome-wide analysis of the ATP-binding cassette (ABC) transporter gene family in sea lamprey and Japanese lamprey</i> . BMC genomics, 16(1), 436.  Crusoe, M. R. et. al. (2015). <i>The khmer software package: enabling efficient nucleotide sequence analysis</i> . F1000Research, 4.  Aleksic, J., Alexa, A., Attwood, T. K., Hong, N. C., Dahlö, M., Davey, R., ..., & Lahti, L. (2014) <i>The open science peer review oath</i> . F1000Research, 3.	
BLOGS AND SOCIAL MEDIA	Professional blog at: <a href="http://camillescott.github.io/blog">camillescott.github.io/blog</a>  Twitter: @camille_codon  Github: <a href="https://github.com/camillescott">github.com/camillescott</a>	
PROFESSIONAL ACTIVITIES	Teaching Assistant (TA) at <b>Alma College</b> , <i>Intro to Computer Science</i>  Co-founder, <b>Alma College Association for Computing Machinery</b>  Lead Instructor/TA at <b>Michigan State University</b> , <i>CSE 101</i>	2011-2012  2012  Fall 2012

Presenter at <b>Michigan State University</b> , <i>Summer Research Opportunities (SROP) Workshop</i>	5/2013
TA for workshop at <b>Marine Biological Laboratory</b> , <i>Strategies and Techniques for Analyzing Microbial Population Structures</i>	8/2013
TA for workshop at <b>California Institute of Technology</b> , <i>Workshop on Microbial Bioinformatics</i>	10/2013
TA for SROP Workshop at <b>Michigan State University</b> , <i>Statistics Bootcamp</i>	05/2014
Participant in Workshop at <b>The Genome Analysis Center (TGAC)</b> , <i>AllBio Open Science &amp; Reproducibility Best Practices Workshop</i>	09/2014
Participant in Workshop at <b>University of California Davis</b> , <i>Software Carpentry "Train the Trainers"</i>	01/2015
Contributor to <b>khmer Protocols Project</b> , <i>Protocols for cloud-based de novo RNA-seq and metagenomic analyses</i> <a href="http://khmer-protocols.readthedocs.org">khmer-protocols.readthedocs.org</a>	
Contributor to open source <b>khmer software package</b> , <i>k-mer counting, graph traversal, and sequence processing</i> <a href="https://github.com/dib-lab/khmer">github.com/dib-lab/khmer</a>	
Author and maintainer of the <b>dammit</b> annotator, <i>a tool for easy de novo transcriptome annotation</i> <a href="https://github.com/camillescott/dammit">github.com/camillescott/dammit</a>	
Author and maintainer of <b>shmlast</b> , <i>an implementation of conditional reciprocal best hits with Python and LAST</i> <a href="https://github.com/camillescott/shmnlst">github.com/camillescott/shmnlst</a>	

REFERENCES      (*Contact details available upon request*)